SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: NATSUKA, SHUNJI
GERSTEN, KEVIN M.
LOWE, JOHN B.

(ii) TITLE OF INVENTION: MURINE ALPHA (1,3) FUCOSYLTRANSFERASE FUC-TVII, DNA ENCODING THE SAME, METHOD FOR PREPARING THE SAME, ANTIBODIES RECOGNIZING THE SAME, IMMUNOASSAYS FOR DETECTING THE SAME, PLASMIDS CONTAINING SUCH DNA

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
(B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
(C) CITY: ARLINGTON
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22202

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/613,098
(B) FILING DATE: 08-MAR-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: LAVALLEYE, JEAN-PAUL
(B) REGISTRATION NUMBER: 31,451
(C) REFERENCE/DOCKET NUMBER: 2363-114-55

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 703-413-3000
(B) TELEFAX: 703-413-2220

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3594 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACAAACAGGA AGGACAGCAG GCTCTGGCAG CCAGAAGCCT GTGGCCCCAA GCTGGCAGGA 60

TGGCCCCCTT CCTGCAGGTC CCCCACAGCC TTCTGGGTTC CTGACACGAG AGAAGAGGTG 120

GGGCGGGGTG AAGTGAACTC TGAAGCCAAA ATGTGACTCT CCTGGGGTCA CCAGCTTGGG 180

GAGAGGTGAA GAAAGATGCC GGGGCGGAAA CAAAGGGGCA GATATCACTA TGGTTATCTT 240

ACTAAGCACA GAGTAACTGA AAAAGCAAGG GTACCGCTGC CCACCTCGTG CCCACCTTAC 300

GTTATACCTC AAACCAGCTA GATAGTTTCT GATGGCACCC ATACCCTCCC TTCCCCTTTA 360

GGCATTGCGC AAGCTCTCCA CCACAATCTG GAAGTTATAC CCTGCGAGGG GATGGGCAGG 420

GCACTTCTGA GGTGCCAATC AGCCTGCACT CGCCTCTGCC CTGGCCATGG CACTGCTGTC 480

AGTTTCTTGG TACCTGTCTC AACAGCAGCC TTGTCACGTG AGACTATGGC TGGCGGTGGG 540

GGTGGGGGCA GGAATCCTAG AAGCACAGGA GTGACATAGG GTCGGGTCGG GCAGAGCGAA 600

GTGTAGGAGG TGATCCCCAA AGGGATGCTG GGGACGATCT GGCCAACACT GTCCTCCCAT 660

TCAAAACTCC CAGTCTGGAG CTCTGGGACA TGGACAAGCC AGGCCTGCTA TTCTCCATAC 720

AGGGCTCCAT AGTGTCTGGC TCAGCAGAGT GGGGGATCTG GTGGGGATGG AGGAAGCTTA 780

GCTAAAAGCT TTGTATAGGC TGAAGCTCTG AGTGACCCTG CTGGGCCACC CTACCCTGGT 840

CTGGGCTGGG TCATTGCATC CCCAGATTGG AAGGCTTGGT GAGATGGAGA GGAACCTTGG 900

CTACAAGCTA TAGCTTTGCC CACCAGAGCC TGCTGGAGGG GAATCAAACA AGCCTGGACC 960

TGAGGCTGGG ACTAGCTTTC CTGTTTCTGG AGTGGATGCC AACCCCCTGC CCACCAGCCT 1020

GCCTGTCCAC GCCAGGGACA CACAGACTCC TTCCCTTTCC AGACTGGAAA GCCCCCTCCT 1080

GGGAGAGCAG GAAGGAAGCA ACCTGCAACT CTTCCAGCCC TGGACCTTGG GCTGAACCTA 1140

CAGTTCAAGG TTTGTATGCT CACAGGTCTT GGCAGGGAAA GATAAGAATC CCCAGGGCAC 1200

CCTCCCCCCC GCCCCCCAGT CCACTGCAGG TAGCTCCTGG GTCTGCCCTT CAGGGCAAGT 1260

GCTGACGCTC CATCAGACTG TGATGGGGCC CTTTTCTGAG GATGACAATT CTGAGAACAA 1320

GGCATTTTTC TAGAGGTGGC AGAACAGCAT TTTGTGATGC CCGAGGATCT GGGAGCACAG 1380

GTCCAGCTTA ATGAGGGATT GGAGGAAGTG GGTATCATCA TTACAGGGAG GGGCCTCTGT 1440

GGCCTCCTGG GAAAATGCAG TTGCTCTCTT TGGGTGGCCT GGGGTTGTGT GGTGGGCAGA 1500

GGACGGAGGT GCTCATTGGG GGAAGGGATC ACTTCTGCTC AGAGTGCTCG CAAGGGCCTT 1560

TCCTTTTCCT GAAGGCAAGC AGGCCTCCTC CTCCTCCTCT TCCTCCTTCT CCTCTTCCTC 1620

CTCTTTCTCC ATATGCCTAG CTGGTCATTT CTAGGGACCA GCATGGTTGG GAAGGGGCC 1680

TTGTCTTGGC CTTCCTCTTG TCTCAATTCC CTCTTTGAGC AGAAGACGGG GTGGGTGGGG 1740

TAGGATTGGA TAGTGGTTGA TGCCAAAGAT TGAAGGGGTA GGGCGGGGCA GAAGTGGGAA 1800

GGTCCCTGGC TTCCTCACCT TGGTAGATGG TGAGGAGCCC CAGAGGTTGA GCTGAGCAGC 1860

AGCTGTGATT TCAGGGTGCC TCTGTTGGAG AGGCTGCTGT GATTTGAAAA TCTTCTTTCC 1920

TTGGTGACAA TTCCAGAAGG CTCCAGATGA ATTGTATTGG TGAGTGCCTG GCCCTTAAGC 1980

AGTCCCAGCT GGGGATGATG GGGATTTATG GGTGTCCCTG AGCCTAGGGT GACAGGGCCT 2040

CTCCTTTTTT TTTTATTCTG CTTCAGGGTA CCACCCCACC AGGAGGCTGC GGGCCTGGGG 2100

CGGCCTAGCT GGAGGAGCAA CATTCATGGT AATTTGGTTT TTCTGGCTGT GGGGATCAGC 2160

TCCTGGAAGT GCCCCTGTGC CTCAGTCCAC ACTCACCATC CTTATCTGGC ACTGGCCTTT 2220

CACCAACCGG CCGCCAGAGC TACCTGGTGA CACCTGCACT CGCTATGGCA TGGCCAGCTG 2280

CCGTCTGAGT GCTAACCGGA GCCTGCTAGC CAGTGCTGAT GCTGTGGTCT TCCACCACCG 2340

TGAGCTGCAA ACCCGGCAAT CTCTCCTACC CCTGGACCAG AGGCCACACG GACAGCCTTG 2400

GGTCTGGGCC TCCATGGAAT CGCCCAGTAA TACCCATGGT CTCCATCGCT TCCGGGGCAT 2460

CTTCAACTGG GTGCTGAGCT ATCGGCGTGA TTCAGATATC TTTGTACCCT ACGGTCGCTT 2520

GCAGCCTCTC TCTGGGCCCA CATCCCCACT ACCGGCCAAA AGCAGGATGG CTGCCTGGGT 2580

GATCAGCAAT TTCCAGGAGC GGCAGCAGCG TGCAAAGCTG TACCGGCAGC TGGCCCCTCA 2640

TCTGCAGGTG GATGTGTTCG GTCGCGCCAG CGGACGGCCC CTATGCGCTA ATTGTCTGCT 2700

GCCCACTTTG GCCCGGTACC GCTTCTACCT GGCCTTTGAG AACTCACAGC ATCGGGACTA 2760

CATCACTGAG AAGTTCTGGC GCAATGCCCT GGCGGCTGGT GCTGTACCCG TGGCGCTGGG 2820

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CTTCAGCTCT GCCCGTGAAC TGGCTGTCTT CCTCGTCAGC ATGAATGAGA GTCGTTATCG 2940

TGGCTTCTTT GCTTGGCGAG ACCGGCTCCG TGTGCGGCTC CTGGGTGACT GGAGGGAGCG 3000

CTTCTGCACC ATCTGTGCCC GCTACCCTTA CTTGCCCCGC AGCCAGGTCT ATGAAGACCT 3060

TGAAAGCTGG TTCCAGGCTT GAACTCCTGC TGCTGGGAGA GGCTGGATGG GTGGGAGACT 3120

GATGTTGAAA CCAAAGAGCT GGGCATCCAG GCTTTTGGTC ACCATGGCAC TACCCCAAGG 3180

CTTTTCCTGT TCAGTGAGCA GGAATTCAGG ATATAAGGAG AAGACTGGGC TGAGATACCC 3240

TGGTGGGCTT TAGAGTAGGG GCCCAGGATA AGAGACAATG AATTAATGAG GAGCATATGG 3300

GGAAGGTGGC TGAGGGTCCC TGACTTACCT TGACCCATGG CTGAAGGCTC CATGCCCATG 3360

GCTGGAGCTG GGACCCTACA CTTCTATAGT CAAGGTGCTT AGCCTCAAGG TTGCAGATGC 3420

ACCCTCTAGT ACTCTGGGTG CAGACTGTAC ACTGGGCGCA GGGGGTTGTG GAAGGACAGT 3480

GCAGATGATT CTGGGCTTTT GACACCACAG TTCCCCCAGG GAAAGAGGCA CTACTAATAA 3540

AAACACTGAC AGAAATCTCC TGGTCAAGTC TGTTAGGCAG CAGAGCTCGA ATTC 3594

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Pro Thr Pro Cys Pro Pro Ala Cys Leu Ser Thr Pro Gly Thr His
1               5                  10                  15

Arg Leu Leu Pro Phe Pro Asp Trp Lys Ala Pro Ser Trp Glu Ser Arg
            20                  25                  30

Lys Glu Ala Thr Cys Asn Ser Ser Ser Pro Gly Pro Trp Ala Glu Pro
        35                  40                  45

Thr Val Gln Met Asn Cys Ile Gly Tyr His Pro Thr Arg Arg Leu Arg
    50                  55                  60

Ala Trp Gly Gly Leu Ala Gly Gly Ala Thr Phe Met Val Ile Trp Phe
65                  70                  75                  80

Phe Trp Leu Trp Gly Ser Ala Pro Gly Ser Ala Pro Val Pro Gln Ser
                85                  90                  95

Thr Leu Thr Ile Leu Ile Trp His Trp Pro Phe Thr Asn Arg Pro Pro
            100                 105                 110

Glu Leu Pro Gly Asp Thr Cys Thr Arg Tyr Gly Met Ala Ser Cys Arg
        115                 120                 125

Leu Ser Ala Asn Arg Ser Leu Leu Ala Ser Ala Asp Ala Val Val Phe
    130                 135                 140

His His Arg Glu Leu Gln Thr Arg Gln Ser Leu Leu Pro Leu Asp Gln
145                 150                 155                 160

Arg Pro His Gly Gln Pro Trp Val Trp Ala Ser Met Glu Ser Pro Ser
                165                 170                 175

Asn Thr His Gly Leu His Arg Phe Arg Gly Ile Phe Asn Trp Val Leu
            180                 185                 190
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Ser Tyr Arg Arg Asp Ser Asp Ile Phe Val Pro Tyr Gly Arg Leu Glu
195 200 205

Pro Leu Ser Gly Pro Thr Ser Pro Leu Pro Ala Lys Ser Arg Met Ala
210 215 220

Ala Trp Val Ile Ser Asn Phe Gln Glu Arg Gln Gln Arg Ala Lys Leu
225 230 235 240

Tyr Arg Gln Leu Ala Pro His Leu Gln Val Asp Val Phe Gly Arg Ala
245 250 255

Ser Gly Arg Pro Leu Cys Ala Asn Cys Leu Leu Pro Thr Leu Ala Arg
260 265 270

Tyr Arg Phe Tyr Leu Ala Phe Glu Asn Ser Gln His Arg Asp Tyr Ile
275 280 285

Thr Glu Lys Phe Trp Arg Asn Ala Leu Ala Ala Gly Ala Val Pro Val
290 295 300

Ala Leu Gly Pro Pro Arg Ala Thr Tyr Glu Ala Phe Val Pro Pro Asp
305 310 315 320

Ala Phe Val His Val Asp Asp Phe Ser Ser Ala Arg Glu Leu Ala Val
325 330 335

Phe Leu Val Ser Met Asn Glu Ser Arg Tyr Arg Gly Phe Phe Ala Trp
340 345 350

Arg Asp Arg Leu Arg Val Arg Leu Leu Gly Asp Trp Arg Glu Arg Phe
355 360 365

Cys Thr Ile Cys Ala Arg Tyr Pro Tyr Leu Pro Arg Ser Gln Val Tyr
370 375 380

Glu Asp Leu Glu Ser Trp Phe Gln Ala
385 390

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "SYNTHETIC PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGCGGATCC CACCATCCTT ATCTGGCACT GGCCTTTCAC C 41

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "SYNTHETIC PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGCGGATCC AGTTCAAGCC TGGAACCAGC TTTCAAGGTC CTTC 44